

SEQUENCE LISTING

<110> Hammer, Philip E.
Hinson, Todd K.
Duck, Nicholas B.
Koziel, Michael G.

<120> METHODS TO CONFER HERBICIDE RESISTANCE

<130> 045600/275110

<150> 60/453,148

<151> 2003-03-10

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2210

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (224)...(1951)

<223> Fungal isolate from soil sample

<400> 1

```
acgcgggggtg cccacggaca acaattccct taggattatc tcctgtattg aatacactct 60
actttgcaac tttacctatt attcgacttt ctttttagagg agcagcattg tcatcattac 120
ctgcccctcc atctgatacc taccttacat tgctcgccaac acacctataa gccataatat 180
accgactcaa agcaaaccac gccattgtt tgattgttta atc atg gcc agc atc 235
                                     Met Ala Ser Ile
                                     1
```

```
aac atc agg gtg cag aat ctc gag caa ccc atg gac gtt gcc gag tat 283
Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp Val Ala Glu Tyr
 5          10          15          20
```

```
ctt ttt cgg cgt ctc cac gaa atc ggc att cgc tcc atc cac ggt ctt 331
Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser Ile His Gly Leu
          25          30          35
```

```
cca ggc gat tac aac ctt ctt gcc ctc gac tat ttg cca tca tgt ggc 379
Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu Pro Ser Cys Gly
          40          45          50
```

```
ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct gct tat gct gct 427
Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala Ala Tyr Ala Ala
          55          60          65
```

gat ggc tat gcc cgc gtc aag cag atg gga gct ctc atc acc act ttt	475
Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu Ile Thr Thr Phe	
70 75 80	
gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc ggt gcc ttt tcg	523
Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala Gly Ala Phe Ser	
85 90 95 100	
gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct tcc act gtc tcg	571
Glu His Val Pro Val Val His Ile Val Gly Cys Pro Ser Thr Val Ser	
105 110 115	
cag cga aac ggc atg ctc ctc cac cac acg ctt gga aac ggc gac ttc	619
Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe	
120 125 130	
aac atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag	667
Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys	
135 140 145	
ctc acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc	715
Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg	
150 155 160	
gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat	763
Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp	
165 170 175 180	
atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac	811
Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp	
185 190 195	
ttg tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac	859
Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp	
200 205 210	
gtt gtc ctc aag tay ctc cgt gct gca aag aac ccc gtc atc ctt gtc	907
Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val	
215 220 225	
gat gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc	955
Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu	
230 235 240	
atc gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt	1003
Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly	
245 250 255 260	
gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac	1051
Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp	
265 270 275	
ggc tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg	1099
Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu	
280 285 290	
ata ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc	1147

Ile	Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn	Thr	Ala	Gly	Phe		
	295						300					305					
tct	tac	cgt	acc	tca	cag	ctg	aac	acg	att	gat	cta	cac	agc	gac	cac	1195	
Ser	Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu	His	Ser	Asp	His		
	310					315					320						
tgc	att	gtc	aaa	tac	tcg	aca	tat	cca	ggc	gtc	cag	atg	agg	ggc	gtg	1243	
Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln	Met	Arg	Gly	Val		
	325					330				335					340		
ctg	cga	caa	gtg	att	aag	cag	ctc	gat	gca	tct	gag	atc	aac	gct	cag	1291	
Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu	Ile	Asn	Ala	Gln		
				345					350					355			
cca	gcg	cca	gtc	gtc	gag	aat	gaa	gtt	gcc	aaa	aac	cga	gat	aac	tca	1339	
Pro	Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser		
			360					365					370				
ccc	gtc	att	aca	caa	gct	ttc	ttc	tgg	ccg	cgc	gtg	gga	gag	ttc	ctg	1387	
Pro	Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu		
		375					380					385					
aag	aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	gcc	aac	ttt	ggc	1435	
Lys	Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly		
	390					395					400						
atc	tgg	gat	act	aag	ttt	ccc	tct	ggc	gtt	act	gcg	ctt	tct	cag	gtc	1483	
Ile	Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val		
	405				410					415					420		
ctt	tgg	gga	agc	att	ggc	tgg	tcc	gtt	ggc	gcc	tgc	caa	gga	gcc	gtt	1531	
Leu	Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val		
				425					430					435			
ctt	gca	gcc	gcc	gat	gac	aac	agc	gat	cgc	aga	act	atc	ctc	ttt	gtt	1579	
Leu	Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val		
			440					445					450				
ggc	gat	ggc	tca	ttc	cag	ctc	act	gct	caa	gaa	ttg	agc	aca	atg	att	1627	
Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile		
		455				460						465					
cgt	ctc	aag	ctg	aag	ccc	atc	atc	ttt	gtc	atc	tgc	aac	gat	ggc	ttt	1675	
Arg	Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe		
	470					475					480						
acc	att	gaa	cga	ttc	att	cac	ggc	atg	gaa	gcc	gag	tac	aac	gac	atc	1723	
Thr	Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile		
	485				490				495						500		
gca	aat	tgg	gac	ttc	aag	gct	ctg	gtt	gac	gtc	ttt	ggc	ggc	tct	aag	1771	
Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys		
				505					510					515			
acg	gcc	aag	aag	ttc	gcc	gtc	aag	acc	aag	gac	gag	ctg	gac	agc	ctt	1819	
Thr	Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu		

520	525	530	
ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc cag ttt gtc gag			1867
Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu			
535	540	545	
cta tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca			1915
Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala			
550	555	560	
gaa gct agc gcg agg aac aat gcc aag aca gag taa agtggactgt			1961
Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *			
565	570	575	
catgaaggcc gatttaccac ctcataaatt gtaatagacc tgatacacat agatcaaggc			2021
aggtaccgat cattaatcaa gcagggtttgg atggggaagg attttgaaaa tgaggaaacg			2081
atgggatgat atttggaata actggccatt attttgagta cttataaaca aatttgaagt			2141
tcaatttttt ttcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			2201
aaaaaaaaa			2210
<210> 2			
<211> 1725			
<212> DNA			
<213> Unknown			
<220>			
<221> CDS			
<222> (1)...(1725)			
<223> Fungal isolate from soil sample			
<400> 2			
atg gcc agc atc aac atc agg gtg cag aat ctc gag caa ccc atg gac			48
Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp			
1	5	10	15
gtt gcc gag tat ctt ttt cgg cgt ctc cac gaa atc ggc att cgc tcc			96
Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser			
20	25	30	
atc cac ggt ctt cca ggc gat tac aac ctt ctt gcc ctc gac tat ttg			144
Ile His Gly Leu Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu			
35	40	45	
cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct			192
Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala			
50	55	60	
gct tat gct gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc			240
Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu			
65	70	75	80
atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc			288
Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala			
85	90	95	

ggt gcc ttt tcg gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct	336
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro	
100 105 110	
tcc act gtc tcg cag cga aac ggc atg ctc ctc cac cac acg ctt gga	384
Ser Thr Val Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly	
115 120 125	
aac ggc gac ttc aac atc ttt gcc aac atg agc gct caa atc tct tgc	432
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys	
130 135 140	
gaa gtg gcc aag ctc acc aac cct gcc gaa att gcg acc cag atc gac	480
Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp	
145 150 155 160	
cat gcc ctc cgc gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg	528
His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met	
165 170 175	
ctt ccc acc gat atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag	576
Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys	
180 185 190	
gaa cca att gac ttg tcg gag cct cca aat gat ccc gag aaa gaa gca	624
Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala	
195 200 205	
tac gtc gtt gac gtt gtc ctc aag tay ctc cgt gct gca aag aac ccc	672
Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro	
210 215 220	
gtc atc ctt gtc gat gct tgt gct atc cgt cat cgt gtt ctt gat gag	720
Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu	
225 230 235 240	
gtt cat gat ctc atc gaa aag aca aac ctc cct gtc ttt gtc act cct	768
Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro	
245 250 255	
atg ggc aaa ggt gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc	816
Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val	
260 265 270	
tat gcc ggt gac ggc tca cat ccg cct caa gtt aag gac atg gtt gag	864
Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu	
275 280 285	
tct tct gat ttg ata ttg aca atc ggt gct ctc aag agc gac ttc aac	912
Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn	
290 295 300	
act gct ggc ttc tct tac cgt acc tca cag ctg aac acg att gat cta	960
Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu	
305 310 315 320	
cac agc gac cac tgc att gtc aaa tac tcg aca tat cca ggt gtc cag	1008

His	Ser	Asp	His	Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln	
				325					330					335		
atg	agg	ggt	gtg	ctg	cga	caa	gtg	att	aag	cag	ctc	gat	gca	tct	gag	1056
Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu	
			340					345					350			
atc	aac	gct	cag	cca	gcg	cca	gtc	gtc	gag	aat	gaa	gtt	gcc	aaa	aac	1104
Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	
		355					360					365				
cga	gat	aac	tca	ccc	gtc	att	aca	caa	gct	ttc	ttc	tgg	ccg	cgc	gtg	1152
Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val	
	370					375					380					
gga	gag	ttc	ctg	aag	aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	1200
Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr	
385					390				395						400	
gcc	aac	ttt	ggc	atc	tgg	gat	act	aag	ttt	ccc	tct	ggc	gtt	act	gcg	1248
Ala	Asn	Phe	Gly	Ile	Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	
			405					410					415			
ctt	tct	cag	gtc	ctt	tgg	gga	agc	att	ggt	tgg	tcc	gtt	ggt	gcc	tgc	1296
Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	
			420					425					430			
caa	gga	gcc	gtt	ctt	gca	gcc	gcc	gat	gac	aac	agc	gat	cgc	aga	act	1344
Gln	Gly	Ala	Val	Leu	Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	
		435					440					445				
atc	ctc	ttt	gtt	ggt	gat	ggc	tca	ttc	cag	ctc	act	gct	caa	gaa	ttg	1392
Ile	Leu	Phe	Val	Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	
	450					455					460					
agc	aca	atg	att	cgt	ctc	aag	ctg	aag	ccc	atc	atc	ttt	gtc	atc	tgc	1440
Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	
465					470				475						480	
aac	gat	ggc	ttt	acc	att	gaa	cga	ttc	att	cac	ggc	atg	gaa	gcc	gag	1488
Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	
			485					490					495			
tac	aac	gac	atc	gca	aat	tgg	gac	ttc	aag	gct	ctg	gtt	gac	gtc	ttt	1536
Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	
			500					505					510			
ggc	ggc	tct	aag	acg	gcc	aag	aag	ttc	gcc	gtc	aag	acc	aag	gac	gag	1584
Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu	
		515					520					525				
ctg	gac	agc	ctt	ctc	aca	gac	cct	acc	ttt	aac	gcc	gca	gaa	tgc	ctc	1632
Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu	
	530					535					540					
cag	ttt	gtc	gag	cta	tat	atg	ccc	aaa	gaa	gat	gct	cct	cga	gca	ttg	1680
Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu	

545	550	555	560	
atc atg act gca gaa gct agc gcg agg aac aat gcc aag aca gag				1725
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu				
	565	570	575	

<210> 3
 <211> 575
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 3
 Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp
 1 5 10 15
 Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser
 20 25 30
 Ile His Gly Leu Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu
 35 40 45
 Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
 50 55 60
 Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
 65 70 75 80
 Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala
 85 90 95
 Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro
 100 105 110
 Ser Thr Val Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly
 115 120 125
 Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys
 130 135 140
 Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp
 145 150 155 160
 His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met
 165 170 175
 Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys
 180 185 190
 Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala
 195 200 205
 Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro
 210 215 220
 Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu
 225 230 235 240
 Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro
 245 250 255
 Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val
 260 265 270
 Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu
 275 280 285
 Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn
 290 295 300
 Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu

305		310		315		320
His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln						
		325		330		335
Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu						
		340		345		350
Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn						
		355		360		365
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val						
		370		375		380
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr						
385		390		395		400
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala						
		405		410		415
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys						
		420		425		430
Gln Gly Ala Val Leu Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr						
		435		440		445
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu						
		450		455		460
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys						
465		470		475		480
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu						
		485		490		495
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe						
		500		505		510
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu						
		515		520		525
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu						
		530		535		540
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu						
545		550		555		560
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu						
		565		570		575

<210> 4
 <211> 835
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (3)...(596)

<223> Fungal isolate from soil sample

<400> 4	
ct ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag aag aac gac atc	47
Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile	
1 5 10 15	
gtc att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag	95
Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys	
20 25 30	
ttt ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att	143

Phe	Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	
			35					40					45			
ggt	tgg	tcc	ggt	ggt	gcc	tgc	caa	gga	gcc	ggt	ctt	gca	gcc	gcc	gat	191
Gly	Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu	Ala	Ala	Ala	Asp	
		50					55				60					
gac	aac	agc	gat	cgc	aga	act	atc	ctc	ttt	ggt	ggt	gat	ggc	tca	ttc	239
Asp	Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly	Asp	Gly	Ser	Phe	
	65					70				75						
cag	ctc	act	gct	caa	gaa	ttg	agc	aca	atg	att	cgt	ctc	aag	ctg	aag	287
Gln	Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	
80					85				90						95	
ccc	atc	atc	ttt	gtc	atc	tgc	aac	gat	ggc	ttt	acc	att	gaa	cga	ttc	335
Pro	Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	
				100					105					110		
att	cac	ggc	atg	gaa	gcc	gag	tac	aac	gac	atc	gca	aat	tgg	gac	ttc	383
Ile	His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	
			115					120					125			
aag	gct	ctg	ggt	gac	gtc	ttt	ggc	ggc	tct	aag	acg	gcc	aag	aag	ttc	431
Lys	Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	
		130					135					140				
gcc	gtc	aag	acc	aag	gac	gag	ctg	gac	agc	ctt	ctc	aca	gac	cct	acc	479
Ala	Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	
		145				150					155					
ttt	aac	gcc	gca	gaa	tgc	ctc	cag	ttt	gtc	gag	cta	tat	atg	ccc	aaa	527
Phe	Asn	Ala	Ala	Glu	Cys	Leu	Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	
160					165				170					175		
gaa	gat	gct	cct	cga	gca	ttg	atc	atg	act	gca	gaa	gct	agc	gcg	agg	575
Glu	Asp	Ala	Pro	Arg	Ala	Leu	Ile	Met	Thr	Ala	Glu	Ala	Ser	Ala	Arg	
				180				185					190			
aac	aat	gcc	aag	aca	gag	taa	agtggactgt	catgaaggcc	gatttaccac							626
Asn	Asn	Ala	Lys	Thr	Glu	*										
			195													
ctcataaatt	gtaatagacc	tgatacacat	agatcaaggc	aggtaccgat	cattaatcaa											686
gcagggtttg	atggggaagg	atgttgaaaa	tgaggaaacg	atgggatgat	atgttggaata											746
actggccatt	atgttgagta	cttataaaca	aatttgaagt	tcaatttttt	ttcaaaaaaa											806
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa														835

<210> 5
 <211> 591
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(591)

<223> Fungal isolate from soil sample

<400> 5

ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag aag aac gac atc gtc	48
Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val	
1 5 10 15	
att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag ttt	96
Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe	
20 25 30	
ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att ggt	144
Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly	
35 40 45	
tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat gac	192
Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp	
50 55 60	
aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc cag	240
Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln	
65 70 75 80	
ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag ccc	288
Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro	
85 90 95	
atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc att	336
Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile	
100 105 110	
cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc aag	384
His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys	
115 120 125	
gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc gcc	432
Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala	
130 135 140	
gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc ttt	480
Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe	
145 150 155 160	
aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa gaa	528
Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu	
165 170 175	
gat gct cct cga gca ttg atc atg act gca gaa gct agc gcg agg aac	576
Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg Asn	
180 185 190	
aat gcc aag aca gag	591
Asn Ala Lys Thr Glu	
195	

<210> 6
 <211> 197
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 6
 Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val
 1 5 10 15
 Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe
 20 25 30
 Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly
 35 40 45
 Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Asp Asp
 50 55 60
 Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln
 65 70 75 80
 Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro
 85 90 95
 Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile
 100 105 110
 His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys
 115 120 125
 Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala
 130 135 140
 Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe
 145 150 155 160
 Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu
 165 170 175
 Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg Asn
 180 185 190
 Asn Ala Lys Thr Glu
 195

<210> 7
 <211> 678
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(678)

<223> Fungal isolate from soil sample

<400> 7
 aca tat cca ggt gtc cag atg agg ggt gtg ctg cga caa gtg att aag 48
 Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu Arg Gln Val Ile Lys
 1 5 10 15
 cag ctc gat gca tct gag atc aac gct cag cca gcg cca gtc gtc gag 96
 Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro Ala Pro Val Val Glu

20	25	30	
aat gaa gtt gcc aaa aac cga gat aac tca ccc gtc att aca caa gct Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro Val Ile Thr Gln Ala 35 40 45			144
ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag aag aac gac atc gtc Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val 50 55 60			192
att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag ttt Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe 65 70 75 80			240
ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att ggt Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly 85 90 95			288
tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat gac Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp 100 105 110			336
aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc cag Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln 115 120 125			384
ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag ccc Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro 130 135 140			432
atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc att Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile 145 150 155 160			480
cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc aag His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys 165 170 175			528
gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc gcc Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala 180 185 190			576
gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc ttt Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe 195 200 205			624
aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa gaa Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu 210 215 220			672
gat gct Asp Ala 225			678

<210> 8
<211> 226

<212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 8
 Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu Arg Gln Val Ile Lys
 1 5 10 15
 Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro Ala Pro Val Val Glu
 20 25 30
 Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro Val Ile Thr Gln Ala
 35 40 45
 Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val
 50 55 60
 Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe
 65 70 75 80
 Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly
 85 90 95
 Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp
 100 105 110
 Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln
 115 120 125
 Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro
 130 135 140
 Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile
 145 150 155 160
 His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys
 165 170 175
 Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala
 180 185 190
 Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe
 195 200 205
 Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu
 210 215 220
 Asp Ala
 225

<210> 9
 <211> 1636
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1377)

<223> Fungal isolate from soil sample

<400> 9
 cga aac ggc atg ctc ctc cac cac acg ctt gga aac ggc gac ttc aac 48
 Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe Asn
 1 5 10 15

atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag ctc	96
Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu	
20 25 30	
acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc gtt	144
Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val	
35 40 45	
tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat atg	192
Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met	
50 55 60	
gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac ttg	240
Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu	
65 70 75 80	
tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac gtt	288
Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val	
85 90 95	
gtc ctc aag tac ctc cgt gct gca aag aac ccc gtc atc ctt gtc gat	336
Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp	
100 105 110	
gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc atc	384
Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile	
115 120 125	
gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt gct	432
Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala	
130 135 140	
gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac ggc	480
Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly	
145 150 155 160	
tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg ata	528
Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile	
165 170 175	
ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc tct	576
Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser	
180 185 190	
tac cgt acc tca cag ctg aac acg att gat cta cac agc gac cac tgc	624
Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys	
195 200 205	
att gtc aaa tac tcg aca tat cca ggt gtc cag atg agg ggt gtg ctg	672
Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu	
210 215 220	
cga caa gtg att aag cag ctc gat gca tct gag atc aac gct cag cca	720
Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro	
225 230 235 240	
gcg cca gtc gtc gag aat gaa gtt gcc aaa aac cga gat aac tca ccc	768

Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser	Pro		
				245					250					255			
gtc	att	aca	caa	gct	ttc	ttc	tgg	ccg	cgc	gtg	gga	gag	ttc	ctg	aag	816	
Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu	Lys		
			260					265					270				
aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	gcc	aac	ttt	ggc	atc	864	
Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly	Ile		
		275					280					285					
tgg	gat	act	aag	ttt	ccc	tct	ggc	gtt	act	gcg	ctt	tct	cag	gtc	ctt	912	
Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu		
	290					295					300						
tgg	gga	agc	att	ggc	tgg	tcc	gtt	ggc	gcc	tgc	caa	gga	gcc	gtt	ctt	960	
Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu		
305					310					315				320			
gca	gcc	gcc	gat	gac	aac	agc	gat	cgc	aga	act	atc	ctc	ttt	gtt	ggc	1008	
Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly		
				325				330						335			
gat	ggc	tca	ttc	cag	ctc	act	gct	caa	gaa	ttg	agc	aca	atg	att	cgt	1056	
Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg		
			340					345					350				
ctc	aag	ctg	aag	ccc	atc	atc	ttt	gtc	atc	tgc	aac	gat	ggc	ttt	acc	1104	
Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr		
		355					360					365					
att	gaa	cga	ttc	att	cac	ggc	atg	gaa	gcc	gag	tac	aac	gac	atc	gca	1152	
Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala		
	370					375					380						
aat	tgg	gac	ttc	aag	gct	ctg	gtt	gac	gtc	ttt	ggc	ggc	tct	aag	acg	1200	
Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr		
385					390					395				400			
gcc	aag	aag	ttc	gcc	gtc	aag	acc	aag	gac	gag	ctg	gac	agc	ctt	ctc	1248	
Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Leu		
				405					410					415			
aca	gac	cct	acc	ttt	aac	gcc	gca	gaa	tgc	ctc	cag	ttt	gtc	gag	cta	1296	
Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu	Gln	Phe	Val	Glu	Leu		
			420					425					430				
tat	atg	ccc	aaa	gaa	gat	gct	cct	cga	gca	ttg	atc	atg	act	gca	gaa	1344	
Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu	Ile	Met	Thr	Ala	Glu		
		435					440					445					
gct	agc	gcg	agg	aac	aat	gcc	aag	aca	gag	taa	agtggactgt	catgaaggcc	1397				
Ala	Ser	Ala	Arg	Asn	Asn	Ala	Lys	Thr	Glu	*							
		450				455											
gatttaccac	ctcataaatt	gtaatagacc	tgatacacat	agatcaaggc	aggtaccgat	1457											
cattaatcaa	gcagggtttgg	atgggggaagg	atgttgaaaa	tgaggaaacg	atgggatgat	1517											

atttggaata actggccatt attttgagta cttataaaca aatttgaagt tcaatttttt 1577
 ttcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1636

<210> 10
 <211> 1374
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1374)

<223> Fungal isolate from soil sample

<400> 10
 cga aac ggc atg ctc ctc cac cac acg ctt gga aac ggc gac ttc aac 48
 Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe Asn
 1 5 10 15
 atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag ctc 96
 Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu
 20 25 30
 acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc gtt 144
 Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val
 35 40 45
 tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat atg 192
 Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met
 50 55 60
 gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac ttg 240
 Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu
 65 70 75 80
 tgc gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac gtt 288
 Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val
 85 90 95
 gtc ctc aag tac ctc cgt gct gca aag aac ccc gtc atc ctt gtc gat 336
 Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp
 100 105 110
 gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc atc 384
 Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile
 115 120 125
 gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt gct 432
 Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala
 130 135 140
 gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac gcc 480
 Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly
 145 150 155 160
 tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg ata 528

Ser	His	Pro	Pro	Gln	Val	Lys	Asp	Met	Val	Glu	Ser	Ser	Asp	Leu	Ile		
				165					170					175			
ttg	aca	atc	ggg	gct	ctc	aag	agc	gac	ttc	aac	act	gct	ggc	ttc	tct	576	
Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn	Thr	Ala	Gly	Phe	Ser		
			180					185					190				
tac	cgt	acc	tca	cag	ctg	aac	acg	att	gat	cta	cac	agc	gac	cac	tgc	624	
Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu	His	Ser	Asp	His	Cys		
		195					200					205					
att	gtc	aaa	tac	tcg	aca	tat	cca	ggg	gtc	cag	atg	agg	ggg	gtg	ctg	672	
Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln	Met	Arg	Gly	Val	Leu		
	210					215					220						
cga	caa	gtg	att	aag	cag	ctc	gat	gca	tct	gag	atc	aac	gct	cag	cca	720	
Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu	Ile	Asn	Ala	Gln	Pro		
225					230					235					240		
gcg	cca	gtc	gtc	gag	aat	gaa	gtt	gcc	aaa	aac	cga	gat	aac	tca	ccc	768	
Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser	Pro		
				245				250						255			
gtc	att	aca	caa	gct	ttc	ttc	tgg	ccg	cgc	gtg	gga	gag	ttc	ctg	aag	816	
Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu	Lys		
			260					265					270				
aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	gcc	aac	ttt	ggc	atc	864	
Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly	Ile		
		275					280				285						
tgg	gat	act	aag	ttt	ccc	tct	ggc	gtt	act	gcg	ctt	tct	cag	gtc	ctt	912	
Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu		
	290					295					300						
tgg	gga	agc	att	ggg	tgg	tcc	gtt	ggg	gcc	tgc	caa	gga	gcc	gtt	ctt	960	
Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu		
305				310				315						320			
gca	gcc	gcc	gat	gac	aac	agc	gat	cgc	aga	act	atc	ctc	ttt	gtt	ggg	1008	
Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly		
				325				330						335			
gat	ggc	tca	ttc	cag	ctc	act	gct	caa	gaa	ttg	agc	aca	atg	att	cgt	1056	
Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg		
			340					345					350				
ctc	aag	ctg	aag	ccc	atc	atc	ttt	gtc	atc	tgc	aac	gat	ggc	ttt	acc	1104	
Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr		
		355					360					365					
att	gaa	cga	ttc	att	cac	ggc	atg	gaa	gcc	gag	tac	aac	gac	atc	gca	1152	
Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala		
	370					375					380						
aat	tgg	gac	ttc	aag	gct	ctg	gtt	gac	gtc	ttt	ggc	ggc	tct	aag	acg	1200	
Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr		

385	390	395	400	
gcc aag aag ttc	gcc gtc aag acc aag	gac gag ctg gac agc ctt ctc	1248	
Ala Lys Lys Phe	Ala Val Lys Thr Lys Asp	Glu Leu Asp Ser Leu Leu		
405	410	415		
aca gac cct acc ttt aac gcc gca gaa tgc ctc cag ttt gtc gag cta	1296			
Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu				
420	425	430		
tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca gaa	1344			
Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu				
435	440	445		
gct agc gcg agg aac aat gcc aag aca gag	1374			
Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu				
450	455			

<210> 11
 <211> 458
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 11
 Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe Asn
 1 5 10 15
 Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu
 20 25 30
 Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val
 35 40 45
 Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met
 50 55 60
 Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu
 65 70 75 80
 Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val
 85 90 95
 Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp
 100 105 110
 Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile
 115 120 125
 Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala
 130 135 140
 Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly
 145 150 155 160
 Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile
 165 170 175
 Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser
 180 185 190
 Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys
 195 200 205
 Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu
 210 215 220

Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu	Ile	Asn	Ala	Gln	Pro
225					230					235					240
Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser	Pro
				245					250					255	
Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu	Lys
			260					265					270		
Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly	Ile
		275					280					285			
Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu
	290					295					300				
Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu
305					310					315					320
Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly
			325					330						335	
Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg
			340					345					350		
Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr
		355					360					365			
Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala
	370					375					380				
Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr
385					390					395					400
Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Leu
			405					410						415	
Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu	Gln	Phe	Val	Glu	Leu
			420					425					430		
Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu	Ile	Met	Thr	Ala	Glu
	435						440					445			
Ala	Ser	Ala	Arg	Asn	Asn	Ala	Lys	Thr	Glu						
	450					455									

<210> 12
 <211> 30
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(30)

<223> Oligonucleotide for PCR amplification of GDC-1

<400> 12
 tcc cag atg cca aag ttg gct gtt cca gtc
 Ser Gln Met Pro Lys Leu Ala Val Pro Val
 1 5 10

30

<210> 13
 <211> 2606
 <212> DNA
 <213> Unknown

<220>
 <221> CDS

<222> (168)...(2258)

<223> Fungal isolate from soil sample

<221> misc_feature

<222> 2370

<223> n = A,T,C or G

<400> 13

```
caattgacga ggagtcgttg ttttcctctt tttctctctc tcccgcacgc cgcgcggtgga 60
ttggggccctt tttatctttt tctgcgatat cctcgactga gaacgacgac gacgagcacg 120
acgacgacga cacaggcgac gactgcgagg cagccccac agccgcc atg atg ctc 176
                                     Met Met Leu
                                     1

cga agt cgc cag gcc tcc aag gcc ctg agg gcc ttg ggc cag gca cgg 224
Arg Ser Arg Gln Ala Ser Lys Ala Leu Arg Ala Leu Gly Gln Ala Arg
      5                      10                      15

cac ttc acc tcg acg aca cag ccc gcc gcc gtg cag gcc ccg aga aag 272
His Phe Thr Ser Thr Thr Gln Pro Ala Ala Val Gln Ala Pro Arg Lys
      20                      25                      30                      35

gtc gcc tcc gga cag cgg aat caa gct acc gcc gcg acg gcc acc tct 320
Val Ala Ser Gly Gln Arg Asn Gln Ala Thr Ala Ala Thr Ala Thr Ser
                        40                      45                      50

gcc gca ccc aat gtc cgc gcc acg ccg agt cct gcc ttc aat gcg gag 368
Ala Ala Pro Asn Val Arg Ala Thr Pro Ser Pro Ala Phe Asn Ala Glu
                        55                      60                      65

gag cag cag cag caa aaa cac agc cat gtc cag ccg ctg gtc aat ccc 416
Glu Gln Gln Gln Gln Lys His Ser His Val Gln Pro Leu Val Asn Pro
                        70                      75                      80

cag aag agc gac atg gat gag tcg ttc atc ggc aag acg ggc ggc gaa 464
Gln Lys Ser Asp Met Asp Glu Ser Phe Ile Gly Lys Thr Gly Gly Glu
                        85                      90                      95

atc ttt cac gaa atg atg ctg aga caa ggc gtc aag cac atc ttt gga 512
Ile Phe His Glu Met Met Leu Arg Gln Gly Val Lys His Ile Phe Gly
      100                      105                      110                      115

tac ccc ggc ggc gcc atc ttg ccc gtc ttc gat gcc atc tac aac tca 560
Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala Ile Tyr Asn Ser
                        120                      125                      130

aaa cac ttc gac ttc atc ctg ccc aga cac gag cag ggc gcc ggc cac 608
Lys His Phe Asp Phe Ile Leu Pro Arg His Glu Gln Gly Ala Gly His
                        135                      140                      145

atg gcc gag ggc tac gcc cgc gcg tcc ggc aag ccc ggc gtc gtc ctc 656
Met Ala Glu Gly Tyr Ala Arg Ala Ser Gly Lys Pro Gly Val Val Leu
                        150                      155                      160

gtc acc tcg ggc ccc ggc gcc acc aac gtc gtg acc cca atg cag gac 704
```

Val	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Val	Val	Thr	Pro	Met	Gln	Asp		
165						170					175						
gcc	ctg	tcc	gac	ggc	acg	cca	ctc	gtc	gtc	ttt	tgc	ggc	cag	gtc	ccg	752	
Ala	Leu	Ser	Asp	Gly	Thr	Pro	Leu	Val	Val	Phe	Cys	Gly	Gln	Val	Pro		
180					185					190					195		
acc	tcg	gcc	atc	ggc	agc	gat	gcc	ttc	cag	gag	gcc	gac	gtc	gtc	ggc	800	
Thr	Ser	Ala	Ile	Gly	Ser	Asp	Ala	Phe	Gln	Glu	Ala	Asp	Val	Val	Gly		
				200					205					210			
atc	tcc	cgc	gcc	tgc	acc	aag	tgg	aac	gtc	atg	gtc	aag	aac	gtc	gcg	848	
Ile	Ser	Arg	Ala	Cys	Thr	Lys	Trp	Asn	Val	Met	Val	Lys	Asn	Val	Ala		
			215					220					225				
gag	ctg	ccg	cgg	aga	atc	aac	gag	gcc	ttt	gag	att	gcc	acg	agc	ggc	896	
Glu	Leu	Pro	Arg	Arg	Ile	Asn	Glu	Ala	Phe	Glu	Ile	Ala	Thr	Ser	Gly		
		230					235					240					
cgc	ccc	ggc	ccc	gtc	ctc	gtc	gac	ctg	ccc	aag	gac	gtc	acc	gcc	ggc	944	
Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Leu	Pro	Lys	Asp	Val	Thr	Ala	Gly		
	245					250					255						
atc	ctg	agg	aga	gcc	atc	ccc	acg	gag	acg	gcc	ctg	ccc	gcg	ctg	ccg	992	
Ile	Leu	Arg	Arg	Ala	Ile	Pro	Thr	Glu	Thr	Ala	Leu	Pro	Ala	Leu	Pro		
260					265					270					275		
agc	gcc	gcc	tcg	cgc	gcc	gcc	atg	gag	tcg	agc	cgg	aaa	cac	ctc	gag	1040	
Ser	Ala	Ala	Ser	Arg	Ala	Ala	Met	Glu	Ser	Ser	Arg	Lys	His	Leu	Glu		
				280					285					290			
cac	acc	atc	aag	cgc	gtc	gcc	gac	ctc	gtc	aac	aag	gcc	aag	cag	cca	1088	
His	Thr	Ile	Lys	Arg	Val	Ala	Asp	Leu	Val	Asn	Lys	Ala	Lys	Gln	Pro		
			295					300					305				
gtc	atc	tac	gcc	ggc	cag	ggc	atc	atc	cag	tcc	gag	ggc	ggg	ccc	gag	1136	
Val	Ile	Tyr	Ala	Gly	Gln	Gly	Ile	Ile	Gln	Ser	Glu	Gly	Gly	Pro	Glu		
		310					315					320					
ctc	ctc	aag	gag	ctg	gcc	gac	aag	gcc	tcc	atc	ccc	gtc	acc	acg	acc	1184	
Leu	Leu	Lys	Glu	Leu	Ala	Asp	Lys	Ala	Ser	Ile	Pro	Val	Thr	Thr	Thr		
		325				330					335						
ctc	cag	ggc	ctc	ggc	ggc	ttc	gac	gag	ctc	gac	gag	aag	tcg	ctg	cac	1232	
Leu	Gln	Gly	Leu	Gly	Gly	Phe	Asp	Glu	Leu	Asp	Glu	Lys	Ser	Leu	His		
340					345					350					355		
atg	ctc	ggc	atg	cac	ggc	tcg	gcc	tac	gcc	aac	atg	gcc	atg	cag	gag	1280	
Met	Leu	Gly	Met	His	Gly	Ser	Ala	Tyr	Ala	Asn	Met	Ala	Met	Gln	Glu		
				360					365					370			
gcc	gac	ctc	atc	atc	gcc	ctc	ggc	gcg	cgc	ttc	gac	gac	cgc	gtc	acc	1328	
Ala	Asp	Leu	Ile	Ile	Ala	Leu	Gly	Ala	Arg	Phe	Asp	Asp	Arg	Val	Thr		
			375					380					385				
ctc	aac	gtg	gcc	aag	ttc	gcg	cct	ggc	gcg	agg	gcc	gcc	gcg	gcc	gag	1376	
Leu	Asn	Val	Ala	Lys	Phe	Ala	Pro	Gly	Ala	Arg	Ala	Ala	Ala	Ala	Glu		

390	395	400	
aag cgc ggc ggc atc gtc cac ttc gag gtg atg ccc aag aac atc aac			1424
Lys Arg Gly Gly Ile Val His Phe Glu Val Met Pro Lys Asn Ile Asn			
405	410	415	
aag gtg gtg cag gcc acc gag gcc gtc gag ggc aac gtc ggc agc aac			1472
Lys Val Val Gln Ala Thr Glu Ala Val Glu Gly Asn Val Gly Ser Asn			
420	425	430	435
ctc aag ctc ctg ctg ccc gag gtg cag gcc aag acg atg gac gac cgc			1520
Leu Lys Leu Leu Leu Pro Glu Val Gln Ala Lys Thr Met Asp Asp Arg			
440	445	450	
aag gag tgg ttc ggc aag atc aac gag tgg aag aag aag tgg ccg ctg			1568
Lys Glu Trp Phe Gly Lys Ile Asn Glu Trp Lys Lys Lys Trp Pro Leu			
455	460	465	
tcg cac tac gag cgt gcg gag cgc cac ggg ctc atc aag ccg cag acc			1616
Ser His Tyr Glu Arg Ala Glu Arg His Gly Leu Ile Lys Pro Gln Thr			
470	475	480	
ctc atc gag gag ctg agc aag ctg acg gcg gac cgc aag gac aag acg			1664
Leu Ile Glu Glu Leu Ser Lys Leu Thr Ala Asp Arg Lys Asp Lys Thr			
485	490	495	
tac att gcc acc ggc gtc gga cag cac cag atg tgg acg gcc cag cac			1712
Tyr Ile Ala Thr Gly Val Gly Gln His Gln Met Trp Thr Ala Gln His			
500	505	510	515
ttc cgg tgg agg cac ccg cgc agc atg atc acg tcg ggt ggt ctc ggc			1760
Phe Arg Trp Arg His Pro Arg Ser Met Ile Thr Ser Gly Gly Leu Gly			
520	525	530	
act atg ggc ttc ggt ctg ccg gct gcc atc ggt gcc aag gtc gcg cag			1808
Thr Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Lys Val Ala Gln			
535	540	545	
ccg gac gcc ctc gtc ttc gat atc gat ggc gac gcg tca ttt ggc atg			1856
Pro Asp Ala Leu Val Phe Asp Ile Asp Gly Asp Ala Ser Phe Gly Met			
550	555	560	
acc ctg acg gag ctg gcc acg gcg gcg cag ttc aac att ggc gtc aag			1904
Thr Leu Thr Glu Leu Ala Thr Ala Ala Gln Phe Asn Ile Gly Val Lys			
565	570	575	
gtc att gtc ctc aac aac gag gag cag ggc atg gta acg cag tgg cag			1952
Val Ile Val Leu Asn Asn Glu Glu Gln Gly Met Val Thr Gln Trp Gln			
580	585	590	595
aac ctc ttc tac gag gac cgc tac gcg cac acg cac cag gtc aac cct			2000
Asn Leu Phe Tyr Glu Asp Arg Tyr Ala His Thr His Gln Val Asn Pro			
600	605	610	
gat ttc atg aag ctg gcc gag tcg atg cgc gtc cag ggc cgg cga tgc			2048
Asp Phe Met Lys Leu Ala Glu Ser Met Arg Val Gln Gly Arg Arg Cys			
615	620	625	

gtg gac ccc gag gac gtg gtc gac agc ctg aag tgg ctg atc aac act 2096
Val Asp Pro Glu Asp Val Val Asp Ser Leu Lys Trp Leu Ile Asn Thr
630 635 640

gac ggc ccg gcc ctg ctg gag gtt gtc acg gac aag aag gtg ccc gtc 2144
Asp Gly Pro Ala Leu Leu Glu Val Val Thr Asp Lys Lys Val Pro Val
645 650 655

ctg ccc atg gtg ccg gcg ggc tcg gcc ctg cac gag ttt ttg gtg ttt 2192
Leu Pro Met Val Pro Ala Gly Ser Ala Leu His Glu Phe Leu Val Phe
660 665 670 675

gac gga gaa aag gac aag aag cga cga gag ctg atg cgg gaa agg acc 2240
Asp Gly Glu Lys Asp Lys Lys Arg Arg Glu Leu Met Arg Glu Arg Thr
680 685 690

tcg ggc ctg cac ggc tag ccgcagcaca cggggcggat tagcagcacc 2288
Ser Gly Leu His Gly *
695

cgacgacggg catccatcca tcaatcatct tctagtcatg ttcttttcat acctcttact 2348
ggcggagttt tgtgcagtta angcaaatcc gggcgcggaag cacaaaaagt tggaggagga 2408
gcagcgccga acggcgggcgc ggtggttagca caggggtggc aatgtgacgg cgggtcgaag 2468
agcccgggca tggcagagta gggcggttgg ttcccatgag gcgagcgagc cgcgcgcggg 2528
cttgcggaag gacacaaaca aacaatgaat gaccattttt ccgagacgtg aaaaaaaaaa 2588
aaaaaaaaa aaaaaaaaaa 2606

<210> 14
<211> 2088
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(2088)

<223> Fungal isolate from soil sample

<400> 14
atg atg ctc cga agt cgc cag gcc tcc aag gcc ctg agg gcc ttg ggc 48
Met Met Leu Arg Ser Arg Gln Ala Ser Lys Ala Leu Arg Ala Leu Gly
1 5 10 15

cag gca cgg cac ttc acc tcg acg aca cag ccc gcc gcc gtg cag gcc 96
Gln Ala Arg His Phe Thr Ser Thr Thr Gln Pro Ala Ala Val Gln Ala
20 25 30

ccg aga aag gtc gcc tcc gga cag cgg aat caa gct acc gcc gcg acg 144
Pro Arg Lys Val Ala Ser Gly Gln Arg Asn Gln Ala Thr Ala Thr
35 40 45

gcc acc tct gcc gca ccc aat gtc cgc gcc acg ccg agt cct gcc ttc 192
Ala Thr Ser Ala Ala Pro Asn Val Arg Ala Thr Pro Ser Pro Ala Phe
50 55 60

aat gcg gag gag cag cag cag caa aaa cac agc cat gtc cag ccg ctg	240
Asn Ala Glu Glu Gln Gln Gln Gln Lys His Ser His Val Gln Pro Leu	
65 70 75 80	
gtc aat ccc cag aag agc gac atg gat gag tcg ttc atc ggc aag acg	288
Val Asn Pro Gln Lys Ser Asp Met Asp Glu Ser Phe Ile Gly Lys Thr	
85 90 95	
ggc ggc gaa atc ttt cac gaa atg atg ctg aga caa ggc gtc aag cac	336
Gly Gly Glu Ile Phe His Glu Met Met Leu Arg Gln Gly Val Lys His	
100 105 110	
atc ttt gga tac ccc ggc ggc gcc atc ttg ccc gtc ttc gat gcc atc	384
Ile Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe Asp Ala Ile	
115 120 125	
tac aac tca aaa cac ttc gac ttc atc ctg ccc aga cac gag cag ggc	432
Tyr Asn Ser Lys His Phe Asp Phe Ile Leu Pro Arg His Glu Gln Gly	
130 135 140	
gcc ggc cac atg gcc gag ggc tac gcc cgc gcg tcc ggc aag ccc ggc	480
Ala Gly His Met Ala Glu Gly Tyr Ala Arg Ala Ser Gly Lys Pro Gly	
145 150 155 160	
gtc gtc ctc gtc acc tcg ggc ccc ggc gcc acc aac gtc gtg acc cca	528
Val Val Leu Val Thr Ser Gly Pro Gly Ala Thr Asn Val Val Thr Pro	
165 170 175	
atg cag gac gcc ctg tcc gac ggc acg cca ctc gtc gtc ttt tgc ggc	576
Met Gln Asp Ala Leu Ser Asp Gly Thr Pro Leu Val Val Phe Cys Gly	
180 185 190	
cag gtc ccg acc tcg gcc atc ggc agc gat gcc ttc cag gag gcc gac	624
Gln Val Pro Thr Ser Ala Ile Gly Ser Asp Ala Phe Gln Glu Ala Asp	
195 200 205	
gtc gtc ggc atc tcc cgc gcc tgc acc aag tgg aac gtc atg gtc aag	672
Val Val Gly Ile Ser Arg Ala Cys Thr Lys Trp Asn Val Met Val Lys	
210 215 220	
aac gtc gcg gag ctg ccg cgg aga atc aac gag gcc ttt gag att gcc	720
Asn Val Ala Glu Leu Pro Arg Arg Ile Asn Glu Ala Phe Glu Ile Ala	
225 230 235 240	
acg agc ggt cgc ccc ggc ccc gtc ctc gtc gac ctg ccc aag gac gtc	768
Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Leu Pro Lys Asp Val	
245 250 255	
acc gcc ggc atc ctg agg aga gcc atc ccc acg gag acg gcc ctg ccc	816
Thr Ala Gly Ile Leu Arg Arg Ala Ile Pro Thr Glu Thr Ala Leu Pro	
260 265 270	
gcg ctg ccg agc gcc gcc tcg cgc gcc gcc atg gag tcg agc cgg aaa	864
Ala Leu Pro Ser Ala Ala Ser Arg Ala Ala Met Glu Ser Ser Arg Lys	
275 280 285	
cac ctc gag cac acc atc aag cgc gtc gcc gac ctc gtc aac aag gcc	912

His	Leu	Glu	His	Thr	Ile	Lys	Arg	Val	Ala	Asp	Leu	Val	Asn	Lys	Ala		
290						295					300						
aag	cag	cca	gtc	atc	tac	gcc	ggc	cag	ggc	atc	atc	cag	tcc	gag	ggc	960	
Lys	Gln	Pro	Val	Ile	Tyr	Ala	Gly	Gln	Gly	Ile	Ile	Gln	Ser	Glu	Gly		
305					310					315					320		
ggg	ccc	gag	ctc	ctc	aag	gag	ctg	gcc	gac	aag	gcc	tcc	atc	ccc	gtc	1008	
Gly	Pro	Glu	Leu	Leu	Lys	Glu	Leu	Ala	Asp	Lys	Ala	Ser	Ile	Pro	Val		
				325					330					335			
acc	acg	acc	ctc	cag	ggc	ctc	ggc	ggc	ttc	gac	gag	ctc	gac	gag	aag	1056	
Thr	Thr	Thr	Leu	Gln	Gly	Leu	Gly	Gly	Phe	Asp	Glu	Leu	Asp	Glu	Lys		
			340					345					350				
tcg	ctg	cac	atg	ctc	ggc	atg	cac	ggc	tcg	gcc	tac	gcc	aac	atg	gcc	1104	
Ser	Leu	His	Met	Leu	Gly	Met	His	Gly	Ser	Ala	Tyr	Ala	Asn	Met	Ala		
		355					360					365					
atg	cag	gag	gcc	gac	ctc	atc	atc	gcc	ctc	ggc	gcg	cgc	ttc	gac	gac	1152	
Met	Gln	Glu	Ala	Asp	Leu	Ile	Ile	Ala	Leu	Gly	Ala	Arg	Phe	Asp	Asp		
	370					375					380						
cgc	gtc	acc	ctc	aac	gtg	gcc	aag	ttc	gcg	cct	ggc	gcg	agg	gcc	gcc	1200	
Arg	Val	Thr	Leu	Asn	Val	Ala	Lys	Phe	Ala	Pro	Gly	Ala	Arg	Ala	Ala		
385					390					395				400			
gcg	gcc	gag	aag	cgc	ggc	ggc	atc	gtc	cac	ttc	gag	gtg	atg	ccc	aag	1248	
Ala	Ala	Glu	Lys	Arg	Gly	Gly	Ile	Val	His	Phe	Glu	Val	Met	Pro	Lys		
				405					410					415			
aac	atc	aac	aag	gtg	gtg	cag	gcc	acc	gag	gcc	gtc	gag	ggc	aac	gtc	1296	
Asn	Ile	Asn	Lys	Val	Val	Gln	Ala	Thr	Glu	Ala	Val	Glu	Gly	Asn	Val		
			420					425					430				
ggc	agc	aac	ctc	aag	ctc	ctg	ctg	ccc	gag	gtg	cag	gcc	aag	acg	atg	1344	
Gly	Ser	Asn	Leu	Lys	Leu	Leu	Leu	Pro	Glu	Val	Gln	Ala	Lys	Thr	Met		
		435					440					445					
gac	gac	cgc	aag	gag	tgg	ttc	ggc	aag	atc	aac	gag	tgg	aag	aag	aag	1392	
Asp	Asp	Arg	Lys	Glu	Trp	Phe	Gly	Lys	Ile	Asn	Glu	Trp	Lys	Lys	Lys		
	450					455					460						
tgg	ccg	ctg	tcg	cac	tac	gag	cgt	gcg	gag	cgc	cac	ggg	ctc	atc	aag	1440	
Trp	Pro	Leu	Ser	His	Tyr	Glu	Arg	Ala	Glu	Arg	His	Gly	Leu	Ile	Lys		
465					470					475				480			
ccg	cag	acc	ctc	atc	gag	gag	ctg	agc	aag	ctg	acg	gcg	gac	cgc	aag	1488	
Pro	Gln	Thr	Leu	Ile	Glu	Glu	Leu	Ser	Lys	Leu	Thr	Ala	Asp	Arg	Lys		
				485					490					495			
gac	aag	acg	tac	att	gcc	acc	ggc	gtc	gga	cag	cac	cag	atg	tgg	acg	1536	
Asp	Lys	Thr	Tyr	Ile	Ala	Thr	Gly	Val	Gly	Gln	His	Gln	Met	Trp	Thr		
			500					505					510				
gcc	cag	cac	ttc	cgg	tgg	agg	cac	ccg	cgc	agc	atg	atc	acg	tcg	ggt	1584	
Ala	Gln	His	Phe	Arg	Trp	Arg	His	Pro	Arg	Ser	Met	Ile	Thr	Ser	Gly		

515	520	525	
ggt ctc ggc act atg ggc ttc ggt ctg ccg gct gcc atc ggt gcc aag Gly Leu Gly Thr Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Lys 530 535 540			1632
gtc gcg cag ccg gac gcc ctc gtc ttc gat atc gat ggc gac gcg tca Val Ala Gln Pro Asp Ala Leu Val Phe Asp Ile Asp Gly Asp Ala Ser 545 550 555 560			1680
ttt ggc atg acc ctg acg gag ctg gcc acg gcg gcg cag ttc aac att Phe Gly Met Thr Leu Thr Glu Leu Ala Thr Ala Ala Gln Phe Asn Ile 565 570 575			1728
ggc gtc aag gtc att gtc ctc aac aac gag gag cag ggc atg gta acg Gly Val Lys Val Ile Val Leu Asn Asn Glu Glu Gln Gly Met Val Thr 580 585 590			1776
cag tgg cag aac ctc ttc tac gag gac cgc tac gcg cac acg cac cag Gln Trp Gln Asn Leu Phe Tyr Glu Asp Arg Tyr Ala His Thr His Gln 595 600 605			1824
gtc aac cct gat ttc atg aag ctg gcc gag tcg atg cgc gtc cag ggc Val Asn Pro Asp Phe Met Lys Leu Ala Glu Ser Met Arg Val Gln Gly 610 615 620			1872
cgg cga tgc gtg gac ccc gag gac gtg gtc gac agc ctg aag tgg ctg Arg Arg Cys Val Asp Pro Glu Asp Val Val Asp Ser Leu Lys Trp Leu 625 630 635 640			1920
atc aac act gac ggc ccg gcc ctg ctg gag gtt gtc acg gac aag aag Ile Asn Thr Asp Gly Pro Ala Leu Leu Glu Val Val Thr Asp Lys Lys 645 650 655			1968
gtg ccc gtc ctg ccc atg gtg ccg gcg ggc tcg gcc ctg cac gag ttt Val Pro Val Leu Pro Met Val Pro Ala Gly Ser Ala Leu His Glu Phe 660 665 670			2016
ttg gtg ttt gac gga gaa aag gac aag aag cga cga gag ctg atg cgg Leu Val Phe Asp Gly Glu Lys Asp Lys Lys Arg Arg Glu Leu Met Arg 675 680 685			2064
gaa agg acc tcg ggc ctg cac ggc Glu Arg Thr Ser Gly Leu His Gly 690 695			2088

<210> 15
 <211> 696
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 15

Met	Met	Leu	Arg	Ser	Arg	Gln	Ala	Ser	Lys	Ala	Leu	Arg	Ala	Leu	Gly
1				5					10					15	
Gln	Ala	Arg	His	Phe	Thr	Ser	Thr	Thr	Gln	Pro	Ala	Ala	Val	Gln	Ala
			20					25					30		
Pro	Arg	Lys	Val	Ala	Ser	Gly	Gln	Arg	Asn	Gln	Ala	Thr	Ala	Ala	Thr
		35					40					45			
Ala	Thr	Ser	Ala	Ala	Pro	Asn	Val	Arg	Ala	Thr	Pro	Ser	Pro	Ala	Phe
	50					55					60				
Asn	Ala	Glu	Glu	Gln	Gln	Gln	Gln	Lys	His	Ser	His	Val	Gln	Pro	Leu
65					70					75					80
Val	Asn	Pro	Gln	Lys	Ser	Asp	Met	Asp	Glu	Ser	Phe	Ile	Gly	Lys	Thr
				85					90					95	
Gly	Gly	Glu	Ile	Phe	His	Glu	Met	Met	Leu	Arg	Gln	Gly	Val	Lys	His
			100					105					110		
Ile	Phe	Gly	Tyr	Pro	Gly	Gly	Ala	Ile	Leu	Pro	Val	Phe	Asp	Ala	Ile
		115					120						125		
Tyr	Asn	Ser	Lys	His	Phe	Asp	Phe	Ile	Leu	Pro	Arg	His	Glu	Gln	Gly
	130					135					140				
Ala	Gly	His	Met	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Ser	Gly	Lys	Pro	Gly
145					150					155					160
Val	Val	Leu	Val	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Val	Val	Thr	Pro
				165					170					175	
Met	Gln	Asp	Ala	Leu	Ser	Asp	Gly	Thr	Pro	Leu	Val	Val	Phe	Cys	Gly
			180					185					190		
Gln	Val	Pro	Thr	Ser	Ala	Ile	Gly	Ser	Asp	Ala	Phe	Gln	Glu	Ala	Asp
		195					200					205			
Val	Val	Gly	Ile	Ser	Arg	Ala	Cys	Thr	Lys	Trp	Asn	Val	Met	Val	Lys
	210					215					220				
Asn	Val	Ala	Glu	Leu	Pro	Arg	Arg	Ile	Asn	Glu	Ala	Phe	Glu	Ile	Ala
225					230					235					240
Thr	Ser	Gly	Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Leu	Pro	Lys	Asp	Val
				245					250					255	
Thr	Ala	Gly	Ile	Leu	Arg	Arg	Ala	Ile	Pro	Thr	Glu	Thr	Ala	Leu	Pro
			260					265					270		
Ala	Leu	Pro	Ser	Ala	Ala	Ser	Arg	Ala	Ala	Met	Glu	Ser	Ser	Arg	Lys
		275					280						285		
His	Leu	Glu	His	Thr	Ile	Lys	Arg	Val	Ala	Asp	Leu	Val	Asn	Lys	Ala
	290					295					300				
Lys	Gln	Pro	Val	Ile	Tyr	Ala	Gly	Gln	Gly	Ile	Ile	Gln	Ser	Glu	Gly
305					310					315					320
Gly	Pro	Glu	Leu	Leu	Lys	Glu	Leu	Ala	Asp	Lys	Ala	Ser	Ile	Pro	Val
				325					330					335	
Thr	Thr	Thr	Leu	Gln	Gly	Leu	Gly	Gly	Phe	Asp	Glu	Leu	Asp	Glu	Lys
			340					345					350		
Ser	Leu	His	Met	Leu	Gly	Met	His	Gly	Ser	Ala	Tyr	Ala	Asn	Met	Ala
		355					360					365			
Met	Gln	Glu	Ala	Asp	Leu	Ile	Ile	Ala	Leu	Gly	Ala	Arg	Phe	Asp	Asp
	370					375					380				
Arg	Val	Thr	Leu	Asn	Val	Ala	Lys	Phe	Ala	Pro	Gly	Ala	Arg	Ala	Ala
385					390					395					400
Ala	Ala	Glu	Lys	Arg	Gly	Gly	Ile	Val	His	Phe	Glu	Val	Met	Pro	Lys
				405					410					415	
Asn	Ile	Asn	Lys	Val	Val	Gln	Ala	Thr	Glu	Ala	Val	Glu	Gly	Asn	Val
			420					425					430		
Gly	Ser	Asn	Leu	Lys	Leu	Leu	Leu	Pro	Glu	Val	Gln	Ala	Lys	Thr	Met
		435					440					445			
Asp	Asp	Arg	Lys	Glu	Trp	Phe	Gly	Lys	Ile	Asn	Glu	Trp	Lys	Lys	Lys

450		455		460											
Trp	Pro	Leu	Ser	His	Tyr	Glu	Arg	Ala	Glu	Arg	His	Gly	Leu	Ile	Lys
465					470					475					480
Pro	Gln	Thr	Leu	Ile	Glu	Glu	Leu	Ser	Lys	Leu	Thr	Ala	Asp	Arg	Lys
				485					490						495
Asp	Lys	Thr	Tyr	Ile	Ala	Thr	Gly	Val	Gly	Gln	His	Gln	Met	Trp	Thr
			500					505					510		
Ala	Gln	His	Phe	Arg	Trp	Arg	His	Pro	Arg	Ser	Met	Ile	Thr	Ser	Gly
		515					520					525			
Gly	Leu	Gly	Thr	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Ile	Gly	Ala	Lys
	530					535					540				
Val	Ala	Gln	Pro	Asp	Ala	Leu	Val	Phe	Asp	Ile	Asp	Gly	Asp	Ala	Ser
545					550				555						560
Phe	Gly	Met	Thr	Leu	Thr	Glu	Leu	Ala	Thr	Ala	Ala	Gln	Phe	Asn	Ile
				565					570						575
Gly	Val	Lys	Val	Ile	Val	Leu	Asn	Asn	Glu	Glu	Gln	Gly	Met	Val	Thr
			580					585					590		
Gln	Trp	Gln	Asn	Leu	Phe	Tyr	Glu	Asp	Arg	Tyr	Ala	His	Thr	His	Gln
		595					600					605			
Val	Asn	Pro	Asp	Phe	Met	Lys	Leu	Ala	Glu	Ser	Met	Arg	Val	Gln	Gly
	610					615					620				
Arg	Arg	Cys	Val	Asp	Pro	Glu	Asp	Val	Val	Asp	Ser	Leu	Lys	Trp	Leu
625					630					635					640
Ile	Asn	Thr	Asp	Gly	Pro	Ala	Leu	Leu	Glu	Val	Val	Thr	Asp	Lys	Lys
			645						650					655	
Val	Pro	Val	Leu	Pro	Met	Val	Pro	Ala	Gly	Ser	Ala	Leu	His	Glu	Phe
		660						665					670		
Leu	Val	Phe	Asp	Gly	Glu	Lys	Asp	Lys	Lys	Arg	Arg	Glu	Leu	Met	Arg
	675						680					685			
Glu	Arg	Thr	Ser	Gly	Leu	His	Gly								
	690					695									

<210> 16
 <211> 563
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 16
Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln
1 5 10 15
Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
20 25 30
Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn
35 40 45
Ala Asn Glu Leu Asn Ala Arg Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
50 55 60
Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80
Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
85 90 95
His Val Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu
100 105 110
Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
115 120 125
Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Cys Thr
130 135 140

Ala	Pro	Ala	Glu	Ile	Asp	Arg	Cys	Ile	Arg	Thr	Thr	Tyr	Val	Thr	Gln
145					150					155					160
Arg	Pro	Val	Tyr	Leu	Gly	Leu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Asn	Val
				165					170						175
Pro	Ala	Lys	Leu	Leu	Gln	Thr	Pro	Ile	Asp	Met	Ser	Leu	Lys	Pro	Asn
			180					185					190		
Asp	Ala	Glu	Ser	Glu	Lys	Glu	Val	Ile	Asp	Thr	Ile	Leu	Val	Leu	Ala
		195					200					205			
Lys	Asp	Ala	Lys	Asn	Pro	Val	Ile	Leu	Ala	Asp	Ala	Cys	Cys	Ser	Arg
	210				215						220				
His	Asp	Val	Lys	Ala	Glu	Thr	Lys	Lys	Leu	Ile	Asp	Leu	Thr	Gln	Phe
225					230					235					240
Pro	Ala	Phe	Val	Thr	Pro	Met	Gly	Lys	Gly	Ser	Ile	Ser	Glu	Gln	His
				245					250						255
Pro	Arg	Tyr	Gly	Gly	Val	Tyr	Val	Gly	Thr	Leu	Ser	Lys	Pro	Glu	Val
			260					265						270	
Lys	Glu	Ala	Val	Glu	Ser	Ala	Asp	Leu	Ile	Leu	Ser	Val	Gly	Ala	Leu
		275					280					285			
Leu	Ser	Asp	Phe	Asn	Thr	Gly	Ser	Phe	Ser	Tyr	Ser	Tyr	Lys	Thr	Lys
	290					295					300				
Asn	Ile	Val	Glu	Phe	His	Ser	Asp	His	Met	Lys	Ile	Arg	Asn	Ala	Thr
305					310					315					320
Phe	Pro	Gly	Val	Gln	Met	Lys	Phe	Val	Leu	Gln	Lys	Leu	Leu	Thr	Asn
				325					330						335
Ile	Ala	Asp	Ala	Ala	Lys	Gly	Tyr	Lys	Pro	Val	Ala	Val	Pro	Ala	Arg
			340					345						350	
Thr	Pro	Ala	Asn	Ala	Ala	Val	Pro	Ala	Ser	Thr	Pro	Leu	Lys	Gln	Glu
		355					360					365			
Trp	Met	Trp	Asn	Gln	Leu	Gly	Asn	Phe	Leu	Gln	Glu	Gly	Asp	Val	Val
	370					375					380				
Ile	Ala	Glu	Thr	Gly	Thr	Ser	Ala	Phe	Gly	Ile	Asn	Gln	Thr	Thr	Phe
385					390					395					400
Pro	Asn	Asn	Thr	Tyr	Gly	Ile	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly
				405					410					415	
Phe	Thr	Thr	Gly	Ala	Thr	Leu	Gly	Ala	Ala	Phe	Ala	Ala	Glu	Glu	Ile
			420					425					430		
Asp	Pro	Lys	Lys	Arg	Val	Ile	Leu	Phe	Ile	Gly	Asp	Gly	Ser	Leu	Gln
		435					440					445			
Leu	Thr	Val	Gln	Glu	Ile	Ser	Thr	Met	Ile	Arg	Trp	Gly	Leu	Lys	Pro
	450					455					460				
Tyr	Leu	Phe	Val	Leu	Asn	Asn	Asp	Gly	Tyr	Thr	Ile	Glu	Lys	Leu	Ile
465					470					475					480
His	Gly	Pro	Lys	Ala	Gln	Tyr	Asn	Glu	Ile	Gln	Gly	Trp	Asp	His	Leu
				485					490					495	
Ser	Leu	Leu	Pro	Thr	Phe	Gly	Ala	Lys	Asp	Tyr	Glu	Thr	His	Arg	Val
			500					505					510		
Ala	Thr	Thr	Gly	Glu	Trp	Asp	Lys	Leu	Thr	Gln	Asp	Lys	Ser	Phe	Asn
		515					520					525			
Asp	Asn	Ser	Lys	Ile	Arg	Met	Ile	Glu	Val	Met	Leu	Pro	Val	Phe	Asp
	530					535					540				
Ala	Pro	Gln	Asn	Leu	Val	Glu	Gln	Ala	Lys	Leu	Thr	Ala	Ala	Thr	Asn
545					550					555					560
Ala	Lys	Gln													

<210> 17

<211> 550
 <212> PRT
 <213> Salmonella typhimurium

<400> 17

Met	Gln	Asn	Pro	Tyr	Thr	Val	Ala	Asp	Tyr	Leu	Leu	Asp	Arg	Leu	Ala
1				5					10					15	
Gly	Cys	Gly	Ile	Gly	His	Leu	Phe	Gly	Val	Pro	Gly	Asp	Tyr	Asn	Leu
			20					25					30		
Gln	Phe	Leu	Asp	His	Val	Ile	Asp	His	Pro	Thr	Leu	Arg	Trp	Val	Gly
	35						40					45			
Cys	Ala	Asn	Glu	Leu	Asn	Ala	Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg
	50					55					60				
Met	Ser	Gly	Ala	Gly	Ala	Leu	Leu	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu
65					70					75					80
Ser	Ala	Ile	Asn	Gly	Ile	Ala	Gly	Ser	Tyr	Ala	Glu	Tyr	Val	Pro	Val
			85						90					95	
Leu	His	Ile	Val	Gly	Ala	Pro	Cys	Ser	Ala	Ala	Gln	Gln	Arg	Gly	Glu
			100					105					110		
Leu	Met	His	His	Thr	Leu	Gly	Asp	Gly	Asp	Phe	Arg	His	Phe	Tyr	Arg
		115				120					125				
Met	Ser	Gln	Ala	Ile	Ser	Ala	Ala	Ser	Ala	Ile	Leu	Asp	Glu	Gln	Asn
	130					135					140				
Ala	Cys	Phe	Glu	Ile	Asp	Arg	Val	Leu	Gly	Glu	Met	Leu	Ala	Ala	Arg
145					150					155					160
Arg	Pro	Gly	Tyr	Ile	Met	Leu	Pro	Ala	Asp	Val	Ala	Lys	Lys	Thr	Ala
				165					170					175	
Ile	Pro	Pro	Thr	Gln	Ala	Leu	Ala	Leu	Pro	Val	His	Glu	Ala	Gln	Ser
			180					185					190		
Gly	Val	Glu	Thr	Ala	Phe	Arg	Tyr	His	Ala	Arg	Gln	Cys	Leu	Met	Asn
	195						200					205			
Ser	Arg	Arg	Ile	Ala	Leu	Leu	Ala	Asp	Phe	Leu	Ala	Gly	Arg	Phe	Gly
	210					215					220				
Leu	Arg	Pro	Leu	Leu	Gln	Arg	Trp	Met	Ala	Glu	Thr	Pro	Ile	Ala	His
225					230					235					240
Ala	Thr	Leu	Leu	Met	Gly	Lys	Gly	Leu	Phe	Asp	Glu	Gln	His	Pro	Asn
				245					250					255	
Phe	Val	Gly	Thr	Tyr	Ser	Ala	Gly	Ala	Ser	Ser	Lys	Glu	Val	Arg	Gln
			260					265					270		
Ala	Ile	Glu	Asp	Ala	Asp	Arg	Val	Ile	Cys	Val	Gly	Thr	Arg	Phe	Val
	275						280					285			
Asp	Thr	Leu	Thr	Ala	Gly	Phe	Thr	Gln	Gln	Leu	Pro	Ala	Glu	Arg	Thr
	290					295					300				
Leu	Glu	Ile	Gln	Pro	Tyr	Ala	Ser	Arg	Ile	Gly	Glu	Thr	Trp	Phe	Asn
305					310					315					320
Leu	Pro	Met	Ala	Gln	Ala	Val	Ser	Thr	Leu	Arg	Glu	Leu	Cys	Leu	Glu
				325					330					335	
Cys	Ala	Phe	Ala	Pro	Pro	Pro	Thr	Arg	Ser	Ala	Gly	Gln	Pro	Val	Arg
			340					345					350		
Ile	Asp	Lys	Gly	Glu	Leu	Thr	Gln	Glu	Ser	Phe	Trp	Gln	Thr	Leu	Gln
		355					360					365			
Gln	Tyr	Leu	Lys	Pro	Gly	Asp	Ile	Ile	Leu	Val	Asp	Gln	Gly	Thr	Ala
	370					375					380				
Ala	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Leu	Pro	Asp	Gly	Ala	Glu	Val	Val
385					390					395					400
Leu	Gln	Pro	Leu	Trp	Gly	Ser	Ile	Gly	Tyr	Ser	Leu	Pro	Ala	Ala	Phe
				405					410					415	

Gly	Ala	Gln	Thr	Ala	Cys	Pro	Asp	Arg	Arg	Val	Ile	Leu	Ile	Ile	Gly
			420					425					430		
Asp	Gly	Ala	Ala	Gln	Leu	Thr	Ile	Gln	Glu	Met	Gly	Ser	Met	Leu	Arg
		435						440				445			
Asp	Gly	Gln	Ala	Pro	Val	Ile	Leu	Leu	Leu	Asn	Asn	Asp	Gly	Tyr	Thr
		450				455					460				
Val	Glu	Arg	Ala	Ile	His	Gly	Ala	Ala	Gln	Arg	Tyr	Asn	Asp	Ile	Ala
465					470					475					480
Ser	Trp	Asn	Trp	Thr	Gln	Ile	Pro	Pro	Ala	Leu	Asn	Ala	Ala	Gln	Gln
				485					490					495	
Ala	Glu	Cys	Trp	Arg	Val	Thr	Gln	Ala	Ile	Gln	Leu	Ala	Glu	Val	Leu
			500					505					510		
Glu	Arg	Leu	Ala	Arg	Pro	Gln	Arg	Leu	Ser	Phe	Ile	Glu	Val	Met	Leu
		515					520					525			
Pro	Lys	Ala	Asp	Leu	Pro	Glu	Leu	Leu	Arg	Thr	Val	Thr	Arg	Ala	Leu
		530				535					540				
Glu	Ala	Arg	Asn	Gly	Gly										
545					550										

<210> 18

<211> 568

<212> PRT

<213> *Zymomonas mobilis*

<400> 18

Met	Ser	Tyr	Thr	Val	Gly	Thr	Tyr	Leu	Ala	Glu	Arg	Leu	Val	Gln	Ile
1				5					10					15	
Gly	Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu
			20					25				30			
Leu	Asp	Asn	Leu	Leu	Leu	Asn	Lys	Asn	Met	Glu	Gln	Val	Tyr	Cys	Cys
		35					40					45			
Asn	Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Lys
		50				55					60				
Gly	Ala	Ala	Ala	Ala	Val	Val	Thr	Tyr	Ser	Val	Gly	Ala	His	Ser	Ala
65					70					75					80
Phe	Asp	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu
				85					90					95	
Ile	Ser	Gly	Ala	Pro	Asn	Asn	Asn	Asp	His	Ala	Ala	Gly	His	Val	Leu
			100					105					110		
His	His	Ala	Leu	Gly	Lys	Thr	Asp	Tyr	His	Tyr	Gln	Leu	Glu	Met	Ala
		115					120					125			
Lys	Asn	Ile	Thr	Ala	Ala	Ala	Glu	Ala	Ile	Tyr	Thr	Pro	Glu	Glu	Ala
		130				135					140				
Pro	Ala	Lys	Ile	Asp	His	Val	Ile	Lys	Thr	Ala	Leu	Ala	Lys	Lys	Lys
145					150					155					160
Pro	Val	Tyr	Leu	Glu	Ile	Ala	Cys	Asn	Ile	Ala	Ser	Met	Pro	Cys	Ala
				165					170					175	
Ala	Pro	Gly	Pro	Ala	Ser	Ala	Leu	Phe	Asn	Asp	Glu	Ala	Ser	Asp	Glu
			180					185					190		
Ala	Ser	Leu	Asn	Ala	Ala	Val	Asp	Glu	Thr	Leu	Lys	Phe	Ile	Ala	Asn
		195					200					205			
Arg	Asp	Lys	Val	Ala	Val	Leu	Val	Gly	Ser	Lys	Leu	Arg	Ala	Ala	Gly
		210				215					220				
Ala	Glu	Glu	Ala	Ala	Val	Lys	Phe	Thr	Asp	Ala	Leu	Gly	Gly	Ala	Val
225					230					235					240
Ala	Thr	Met	Ala	Ala	Ala	Lys	Ser	Phe	Phe	Pro	Glu	Glu	Asn	Pro	His

Pro	Leu	Glu	Gln	Pro	Ala	Glu	Pro	Ser	Lys	Leu	Ala	Lys	Lys	Leu	Arg
65					70					75					80
Ala	Glu	Pro	Asp	Met	Asp	Thr	Ser	Phe	Val	Gly	Leu	Thr	Gly	Gly	Gln
				85					90					95	
Ile	Phe	Asn	Glu	Met	Met	Ser	Arg	Gln	Asn	Val	Asp	Thr	Val	Phe	Gly
			100					105					110		
Tyr	Pro	Gly	Gly	Ala	Ile	Leu	Pro	Val	Tyr	Asp	Ala	Ile	His	Asn	Ser
		115					120					125			
Asp	Lys	Phe	Asn	Phe	Val	Leu	Pro	Lys	His	Glu	Gln	Gly	Ala	Gly	His
	130					135					140				
Met	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Ser	Gly	Lys	Pro	Gly	Val	Val	Leu
145					150					155					160
Val	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Val	Val	Thr	Pro	Met	Ala	Asp
				165					170					175	
Ala	Phe	Ala	Asp	Gly	Ile	Pro	Met	Val	Val	Phe	Thr	Gly	Gln	Val	Pro
			180					185					190		
Thr	Ser	Ala	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Ala	Asp	Val	Val	Gly
		195					200					205			
Ile	Ser	Arg	Ser	Cys	Thr	Lys	Trp	Asn	Val	Met	Val	Lys	Ser	Val	Glu
	210					215					220				
Glu	Leu	Pro	Leu	Arg	Ile	Asn	Glu	Ala	Phe	Glu	Ile	Ala	Thr	Ser	Gly
225					230					235					240
Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Leu	Pro	Lys	Asp	Val	Thr	Ala	Ala
				245					250					255	
Ile	Leu	Arg	Asn	Pro	Ile	Pro	Thr	Lys	Thr	Thr	Leu	Pro	Ser	Asn	Ala
			260					265					270		
Leu	Asn	Gln	Leu	Thr	Ser	Arg	Ala	Gln	Asp	Glu	Phe	Val	Met	Gln	Ser
	275						280					285			
Ile	Asn	Lys	Ala	Ala	Asp	Leu	Ile	Asn	Leu	Ala	Lys	Lys	Pro	Val	Leu
	290					295					300				
Tyr	Val	Gly	Ala	Gly	Ile	Leu	Asn	His	Ala	Asp	Gly	Pro	Arg	Leu	Leu
305					310					315					320
Lys	Glu	Leu	Ser	Asp	Arg	Ala	Gln	Ile	Pro	Val	Thr	Thr	Thr	Leu	Gln
				325					330					335	
Gly	Leu	Gly	Ser	Phe	Asp	Gln	Glu	Asp	Pro	Lys	Ser	Leu	Asp	Met	Leu
			340					345					350		
Gly	Met	His	Gly	Cys	Ala	Thr	Ala	Asn	Leu	Ala	Val	Gln	Asn	Ala	Asp
		355					360					365			
Leu	Ile	Ile	Ala	Val	Gly	Ala	Arg	Phe	Asp	Asp	Arg	Val	Thr	Gly	Asn
	370					375					380				
Ile	Ser	Lys	Phe	Ala	Pro	Glu	Ala	Arg	Arg	Ala	Ala	Ala	Glu	Gly	Arg
385					390					395					400
Gly	Gly	Ile	Ile	His	Phe	Glu	Val	Ser	Pro	Lys	Asn	Ile	Asn	Lys	Val
				405					410					415	
Val	Gln	Thr	Gln	Ile	Ala	Val	Glu	Gly	Asp	Ala	Thr	Thr	Asn	Leu	Gly
			420					425					430		
Lys	Met	Met	Ser	Lys	Ile	Phe	Pro	Val	Lys	Glu	Arg	Ser	Glu	Trp	Phe
		435					440					445			
Ala	Gln	Ile	Asn	Lys	Trp	Lys	Lys	Glu	Tyr	Pro	Tyr	Ala	Tyr	Met	Glu
	450					455					460				
Glu	Thr	Pro	Gly	Ser	Lys	Ile	Lys	Pro	Gln	Thr	Val	Ile	Lys	Lys	Leu
465					470					475					480
Ser	Lys	Val	Ala	Asn	Asp	Thr	Gly	Arg	His	Val	Ile	Val	Thr	Thr	Gly
				485					490					495	
Val	Gly	Gln	His	Gln	Met	Trp	Ala	Ala	Gln	His	Trp	Thr	Trp	Arg	Asn
			500					505					510		
Pro	His	Thr	Phe	Ile	Thr	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Gly

Glu	Ile	Ala	Thr	Ser	Gly	Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Pro	Ala
225					230					235					240
Lys	Asp	Val	Thr	Ala	Ser	Val	Leu	Arg	Arg	Ala	Ile	Pro	Thr	Glu	Thr
				245						250					255
Ser	Ile	Pro	Ser	Ile	Ser	Ala	Ala	Ala	Arg	Ala	Val	Gln	Glu	Ala	Gly
			260						265						270
Arg	Lys	Gln	Leu	Glu	His	Ser	Ile	Lys	Arg	Val	Ala	Asp	Leu	Val	Asn
		275							280						285
Ile	Ala	Lys	Lys	Pro	Val	Ile	Tyr	Ala	Gly	Gln	Gly	Val	Ile	Leu	Ser
	290						295					300			
Glu	Gly	Gly	Val	Glu	Leu	Lys	Ala	Leu	Ala	Asp	Lys	Ala	Ser	Ile	
305					310					315					320
Pro	Val	Thr	Thr	Thr	Leu	His	Gly	Leu	Gly	Ala	Phe	Asp	Glu	Leu	Asp
				325						330					335
Glu	Lys	Ala	Leu	His	Met	Leu	Gly	Met	His	Gly	Ser	Ala	Tyr	Ala	Asn
			340							345					350
Met	Ser	Met	Gln	Glu	Ala	Asp	Leu	Ile	Ile	Ala	Leu	Gly	Gly	Arg	Phe
		355								360					365
Asp	Asp	Arg	Val	Thr	Gly	Ser	Ile	Pro	Lys	Phe	Ala	Pro	Ala	Ala	Lys
	370						375					380			
Leu	Ala	Ala	Ala	Glu	Gly	Arg	Gly	Gly	Ile	Val	His	Phe	Glu	Ile	Met
385					390						395				400
Pro	Lys	Asn	Ile	Asn	Lys	Val	Val	Gln	Ala	Thr	Glu	Ala	Ile	Glu	Gly
				405						410					415
Asp	Val	Ala	Ser	Asn	Leu	Lys	Leu	Leu	Leu	Pro	Lys	Ile	Glu	Gln	Arg
			420							425					430
Ser	Met	Thr	Asp	Arg	Lys	Glu	Trp	Phe	Asp	Gln	Ile	Lys	Glu	Trp	Lys
		435								440					445
Glu	Lys	Trp	Pro	Leu	Ser	His	Tyr	Glu	Arg	Ala	Glu	Arg	Ser	Gly	Leu
	450						455								460
Ile	Lys	Pro	Gln	Thr	Leu	Ile	Glu	Glu	Leu	Ser	Asn	Leu	Thr	Ala	Asp
465						470					475				480
Arg	Lys	Asp	Met	Thr	Tyr	Ile	Thr	Thr	Gly	Val	Gly	Gln	His	Gln	Met
				485							490				495
Trp	Thr	Ala	Gln	His	Phe	Arg	Trp	Arg	His	Pro	Arg	Ser	Met	Ile	Thr
			500							505					510
Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Gly	Leu	Pro	Ala	Ala	Ile	Gly
		515								520					525
Ala	Lys	Val	Ala	Arg	Pro	Asp	Ala	Leu	Val	Ile	Asp	Ile	Asp	Gly	Asp
							535					540			
Ala	Ser	Phe	Asn	Met	Thr	Leu	Thr	Glu	Leu	Ser	Thr	Ala	Ala	Gln	Phe
545							550				555				560
Asn	Ile	Gly	Val	Lys	Val	Ile	Val	Leu	Asn	Asn	Glu	Glu	Gln	Gly	Met
				565							570				575
Val	Thr	Gln	Trp	Gln	Asn	Leu	Phe	Tyr	Glu	Asp	Arg	Tyr	Ser	His	Thr
			580							585					590
His	Gln	Arg	Asn	Pro	Asp	Phe	Met	Lys	Leu	Ala	Asp	Ala	Met	Asp	Val
		595						600					605		
Gln	His	Arg	Arg	Val	Ser	Lys	Pro	Asp	Asp	Val	Gly	Asp	Ala	Leu	Thr
	610						615					620			
Trp	Leu	Ile	Asn	Thr	Asp	Gly	Pro	Ala	Leu	Leu	Glu	Val	Met	Thr	Asp
625						630					635				640
Lys	Lys	Val	Pro	Val	Leu	Pro	Met	Val	Pro	Gly	Gly	Asn	Gly	Leu	His
				645							650				655
Glu	Phe	Ile	Thr	Phe	Asp	Ala	Ser	Lys	Asp	Lys	Gln	Arg	Arg	Glu	Leu
			660						665						670
Met	Arg	Ala	Arg	Thr	Asn	Gly	Leu	His	Gly	Arg	Thr	Ala	Val		

675

680

685

<210> 21
 <211> 1728
 <212> DNA
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<221> CDS
 <222> (1)...(1728)

<400> 21
 atg gcc agc atc aac atc agg gtg cag aat ctc gag caa ccc atg gac 48
 Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp
 1 5 10 15
 gtt gcc gag tat ctt ttc cgg cgt ctc cac gaa atc ggc att cgc tcc 96
 Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser
 20 25 30
 atc cac ggt ctt cca ggc gat tac aac cct ctt gcc ctc gac tat ttg 144
 Ile His Gly Leu Pro Gly Asp Tyr Asn Pro Leu Ala Leu Asp Tyr Leu
 35 40 45
 cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct 192
 Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
 50 55 60
 gct tat gct gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc 240
 Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
 65 70 75 80
 atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc 288
 Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala
 85 90 95
 ggt gcc ttt tcg gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct 336
 Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro
 100 105 110
 tcc act gcc tcg cag cga aac ggc atg ctc ctc cac cac acg ctt gga 384
 Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly
 115 120 125
 aac ggc gac ttc aac atc ttt gcc aac atg agc gct caa atc tct tgc 432
 Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys
 130 135 140
 gaa gtg gcc aag ctc acc aac cct gcc gaa att gcg acc cag atc gac 480
 Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp
 145 150 155 160
 cat gcc ctc cgc gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg 528
 His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met

165										170					175					
ctt	ccc	acc	gat	atg	gtc	cag	gcc	aaa	gta	gaa	ggt	gcc	aga	ctc	aag	576				
Leu	Pro	Thr	Asp	Met	Val	Gln	Ala	Lys	Val	Glu	Gly	Ala	Arg	Leu	Lys					
			180						185			190								
gaa	cca	att	gac	ttg	tcg	gag	cct	cca	aat	gat	ccc	gag	aaa	gaa	gca	624				
Glu	Pro	Ile	Asp	Leu	Ser	Glu	Pro	Pro	Asn	Asp	Pro	Glu	Lys	Glu	Ala					
			195						200			205								
tac	gtc	gtt	gac	gtt	gtc	ctc	aag	tac	ctc	cgt	gct	gca	aag	aac	ccc	672				
Tyr	Val	Val	Asp	Val	Val	Leu	Lys	Tyr	Leu	Arg	Ala	Ala	Lys	Asn	Pro					
			210						215			220								
gtc	atc	ctt	gtc	gat	gct	tgt	gct	atc	cgt	cat	cgt	gtt	ctt	gat	gag	720				
Val	Ile	Leu	Val	Asp	Ala	Cys	Ala	Ile	Arg	His	Arg	Val	Leu	Asp	Glu					
225						230						235			240					
gtt	cat	gat	ctc	atc	gaa	aag	aca	aac	ctc	ccc	gtc	ttt	gtc	act	cct	768				
Val	His	Asp	Leu	Ile	Glu	Lys	Thr	Asn	Leu	Pro	Val	Phe	Val	Thr	Pro					
			245						250			255								
atg	ggc	aaa	ggt	gct	gtt	aac	gaa	gaa	cac	ccg	aca	tat	ggt	ggt	gtc	816				
Met	Gly	Lys	Gly	Ala	Val	Asn	Glu	Glu	His	Pro	Thr	Tyr	Gly	Gly	Val					
			260						265			270								
tat	gcc	ggt	gac	ggc	tca	cat	ccg	cct	caa	gtt	aag	gac	atg	gtt	gag	864				
Tyr	Ala	Gly	Asp	Gly	Ser	His	Pro	Pro	Gln	Val	Lys	Asp	Met	Val	Glu					
			275						280			285								
tct	tct	gat	ttg	ata	ttg	aca	atc	ggt	gct	ctc	aag	agc	gac	ttc	aac	912				
Ser	Ser	Asp	Leu	Ile	Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn					
			290						295			300								
act	gct	ggc	ttc	tct	tac	cgt	acc	tca	cag	ctg	aac	acg	att	gat	cta	960				
Thr	Ala	Gly	Phe	Ser	Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu					
305						310						315			320					
cac	agc	gac	cac	tgc	att	gtc	aaa	tac	tcg	aca	tat	cca	ggt	gtc	cag	1008				
His	Ser	Asp	His	Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln					
			325						330			335								
atg	agg	ggt	gtg	ctg	cga	caa	gtg	att	aag	cag	ctc	gat	gca	tct	gag	1056				
Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu					
			340						345			350								
atc	aac	gct	cag	cca	gcg	cca	gtc	gtc	gag	aat	gaa	gtt	gcc	aaa	aac	1104				
Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn					
			355						360			365								
cga	gat	aac	tca	ccc	gtc	att	aca	caa	gct	ttc	ttc	tggt	ccg	cgc	gtg	1152				
Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val					
			370						375			380								
gga	gag	ttc	ctg	aag	aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	1200				
Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr					
385						390						395			400					

gcc aac ttt ggc atc tgg gat act aag ttt ccc tct ggc gtt act gcg	1248
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala	
405 410 415	
ctt tct cag gtc ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc	1296
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys	
420 425 430	
caa gga gcc gtt ctt gca gcc gcc gat gac aac agc gat cgc aga act	1344
Gln Gly Ala Val Leu Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr	
435 440 445	
atc ctc ttt gtt ggt gat ggc tca ttc cag ctc act gct caa gaa ttg	1392
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu	
450 455 460	
agc aca atg att cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc	1440
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys	
465 470 475 480	
aac gat ggc ttt acc att gaa cga ttc att cac ggc atg gaa gcc gag	1488
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu	
485 490 495	
tac aac gac atc gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt	1536
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe	
500 505 510	
ggc ggc tct aag acg gcc aag aag ttc gcc gtc aag acc aag gac gag	1584
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu	
515 520 525	
ctg gac agc ctt ctg aca gac cct acc ttt aac gcc gca gaa tgc ctc	1632
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu	
530 535 540	
cag ttt gtc gag cta tat atg ccc aaa gaa gat gct cct cga gca ttg	1680
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu	
545 550 555 560	
atc atg acg gca gaa gct agc gcg agg aac aat gcc aag aca gag taa	1728
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *	
565 570 575	

<210> 22

<211> 575

<212> PRT

<213> Unknown

<220>

<223> Fungal isolate from soil sample

<400> 22

Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp

1	5							10							15						
Val	Ala	Glu	Tyr	Leu	Phe	Arg	Arg	Leu	His	Glu	Ile	Gly	Ile	Arg	Ser						
			20					25					30								
Ile	His	Gly	Leu	Pro	Gly	Asp	Tyr	Asn	Pro	Leu	Ala	Leu	Asp	Tyr	Leu						
		35					40					45									
Pro	Ser	Cys	Gly	Leu	Arg	Trp	Val	Gly	Ser	Val	Asn	Glu	Leu	Asn	Ala						
		50				55					60										
Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg	Val	Lys	Gln	Met	Gly	Ala	Leu						
65				70					75					80							
Ile	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala	Ile	Asn	Gly	Val	Ala						
			85					90					95								
Gly	Ala	Phe	Ser	Glu	His	Val	Pro	Val	Val	His	Ile	Val	Gly	Cys	Pro						
			100				105					110									
Ser	Thr	Ala	Ser	Gln	Arg	Asn	Gly	Met	Leu	Leu	His	His	Thr	Leu	Gly						
		115				120					125										
Asn	Gly	Asp	Phe	Asn	Ile	Phe	Ala	Asn	Met	Ser	Ala	Gln	Ile	Ser	Cys						
		130				135					140										
Glu	Val	Ala	Lys	Leu	Thr	Asn	Pro	Ala	Glu	Ile	Ala	Thr	Gln	Ile	Asp						
145				150					155					160							
His	Ala	Leu	Arg	Val	Cys	Phe	Ile	Arg	Ser	Arg	Pro	Val	Tyr	Ile	Met						
			165					170					175								
Leu	Pro	Thr	Asp	Met	Val	Gln	Ala	Lys	Val	Glu	Gly	Ala	Arg	Leu	Lys						
			180			185						190									
Glu	Pro	Ile	Asp	Leu	Ser	Glu	Pro	Pro	Asn	Asp	Pro	Glu	Lys	Glu	Ala						
		195				200					205										
Tyr	Val	Val	Asp	Val	Val	Leu	Lys	Tyr	Leu	Arg	Ala	Ala	Lys	Asn	Pro						
	210					215				220											
Val	Ile	Leu	Val	Asp	Ala	Cys	Ala	Ile	Arg	His	Arg	Val	Leu	Asp	Glu						
225				230					235					240							
Val	His	Asp	Leu	Ile	Glu	Lys	Thr	Asn	Leu	Pro	Val	Phe	Val	Thr	Pro						
			245					250					255								
Met	Gly	Lys	Gly	Ala	Val	Asn	Glu	Glu	His	Pro	Thr	Tyr	Gly	Gly	Val						
			260				265					270									
Tyr	Ala	Gly	Asp	Gly	Ser	His	Pro	Pro	Gln	Val	Lys	Asp	Met	Val	Glu						
		275				280					285										
Ser	Ser	Asp	Leu	Ile	Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn						
	290					295					300										
Thr	Ala	Gly	Phe	Ser	Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu						
305				310					315					320							
His	Ser	Asp	His	Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln						
			325					330					335								
Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu						
			340				345					350									
Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala								

Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys
465					470				475						480
Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu
				485					490						495
Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe
			500					505						510	
Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu
		515					520					525			
Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu
	530					535					540				
Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu
545					550					555					560
Ile	Met	Thr	Ala	Glu	Ala	Ser	Ala	Arg	Asn	Asn	Ala	Lys	Thr	Glu	
				565					570					575	

<210> 23

<211> 1728

<212> DNA

<213> Unknown

<220>

<223> Fungal isolate from soil sample

<221> CDS

<222> (1)...(1728)

<400> 23

atg	gcc	agc	atc	aac	atc	agg	gtg	cag	aat	ctc	gag	caa	ccc	atg	gac	48
Met	Ala	Ser	Ile	Asn	Ile	Arg	Val	Gln	Asn	Leu	Glu	Gln	Pro	Met	Asp	
1				5					10					15		
gtt	gcc	gag	tat	ctt	ttc	cgg	cgt	ctc	cac	gaa	atc	ggc	att	cgc	tcc	96
Val	Ala	Glu	Tyr	Leu	Phe	Arg	Arg	Leu	His	Glu	Ile	Gly	Ile	Arg	Ser	
			20					25					30			
atc	cac	ggt	ctt	cca	ggc	gat	tac	aac	ctt	ctt	gcc	ctc	gac	tat	ttg	144
Ile	His	Gly	Leu	Pro	Gly	Asp	Tyr	Asn	Leu	Leu	Ala	Leu	Asp	Tyr	Leu	
		35				40						45				
cca	tca	tgt	ggc	ctg	aga	tgg	gtt	ggc	agc	gtc	aac	gaa	ctc	aat	gct	192
Pro	Ser	Cys	Gly	Leu	Arg	Trp	Val	Gly	Ser	Val	Asn	Glu	Leu	Asn	Ala	
	50					55					60					
gct	tat	gct	gct	gat	ggc	tat	gcc	cgc	gtc	aag	cag	atg	gga	gct	ctc	240
Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ala	Arg	Val	Lys	Gln	Met	Gly	Ala	Leu	
65				70					75					80		
atc	acc	act	ttt	gga	gtg	gga	gag	ctc	tca	gcc	atc	aat	ggc	gtt	gcc	288
Ile	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala	Ile	Asn	Gly	Val	Ala	
			85					90						95		
ggt	gcc	ttt	tcg	gaa	cac	gtc	cca	gtc	gtt	cac	att	gtt	ggc	tcg	cct	336
Gly	Ala	Phe	Ser	Glu	His	Val	Pro	Val	Val	His	Ile	Val	Gly	Cys	Pro	
			100					105					110			
tcc	act	gcc	tcg	cag	cga	aac	ggc	atg	ctc	ctc	cac	cac	acg	ctt	gga	384

Ser	Thr	Ala	Ser	Gln	Arg	Asn	Gly	Met	Leu	Leu	His	His	Thr	Leu	Gly		
		115					120					125					
aac	ggc	gac	ttc	aac	atc	ttt	gcc	aac	atg	agc	gct	caa	atc	tct	tgc	432	
Asn	Gly	Asp	Phe	Asn	Ile	Phe	Ala	Asn	Met	Ser	Ala	Gln	Ile	Ser	Cys		
		130				135					140						
gaa	gtg	gcc	aag	ctc	acc	aac	cct	gcc	gaa	att	gcg	acc	cag	atc	gac	480	
Glu	Val	Ala	Lys	Leu	Thr	Asn	Pro	Ala	Glu	Ile	Ala	Thr	Gln	Ile	Asp		
		145				150					155				160		
cat	gcc	ctc	cgc	gtt	tgc	ttc	att	cgt	tct	cgg	ccc	gtc	tac	atc	atg	528	
His	Ala	Leu	Arg	Val	Cys	Phe	Ile	Arg	Ser	Arg	Pro	Val	Tyr	Ile	Met		
				165					170						175		
ctt	ccc	acc	gat	atg	gtc	cag	gcc	aaa	gta	gaa	ggg	gcc	aga	ctc	aag	576	
Leu	Pro	Thr	Asp	Met	Val	Gln	Ala	Lys	Val	Glu	Gly	Ala	Arg	Leu	Lys		
			180					185					190				
gaa	cca	att	gac	ttg	tcg	gag	cct	cca	aat	gat	ccc	gag	aaa	gaa	gca	624	
Glu	Pro	Ile	Asp	Leu	Ser	Glu	Pro	Pro	Asn	Asp	Pro	Glu	Lys	Glu	Ala		
		195					200					205					
tac	gtc	gtt	gac	gtt	gtc	ctc	aag	tac	ctc	cgt	gct	gca	aag	aac	ccc	672	
Tyr	Val	Val	Asp	Val	Val	Leu	Lys	Tyr	Leu	Arg	Ala	Ala	Lys	Asn	Pro		
		210				215					220						
gtc	atc	ctt	gtc	gat	gct	tgt	gct	atc	cgt	cat	cgt	gtt	ctt	gat	gag	720	
Val	Ile	Leu	Val	Asp	Ala	Cys	Ala	Ile	Arg	His	Arg	Val	Leu	Asp	Glu		
		225				230				235					240		
gtt	cat	gat	ctc	atc	gaa	aag	aca	aac	ctc	ccc	gtc	ttt	gtc	act	cct	768	
Val	His	Asp	Leu	Ile	Glu	Lys	Thr	Asn	Leu	Pro	Val	Phe	Val	Thr	Pro		
				245					250					255			
atg	ggc	aaa	ggg	gct	gtt	aac	gaa	gaa	cac	ccg	aca	tat	ggg	ggg	gtc	816	
Met	Gly	Lys	Gly	Ala	Val	Asn	Glu	Glu	His	Pro	Thr	Tyr	Gly	Gly	Val		
			260					265					270				
tat	gcc	ggg	gac	ggc	tca	cat	ccg	cct	caa	gtt	aag	gac	atg	gtt	gag	864	
Tyr	Ala	Gly	Asp	Gly	Ser	His	Pro	Pro	Gln	Val	Lys	Asp	Met	Val	Glu		
		275					280					285					
tct	tct	gat	ttg	ata	ttg	aca	atc	ggg	gct	ctc	aag	agc	gac	ttc	aac	912	
Ser	Ser	Asp	Leu	Ile	Leu	Thr	Ile	Gly	Ala	Leu	Lys	Ser	Asp	Phe	Asn		
		290				295					300						
act	gct	ggc	ttc	tct	tac	cgt	acc	tca	cag	ctg	aac	acg	att	gat	cta	960	
Thr	Ala	Gly	Phe	Ser	Tyr	Arg	Thr	Ser	Gln	Leu	Asn	Thr	Ile	Asp	Leu		
		305				310				315					320		
cac	agc	gac	cac	tgc	att	gtc	aaa	tac	tcg	aca	tat	cca	ggg	gtc	cag	1008	
His	Ser	Asp	His	Cys	Ile	Val	Lys	Tyr	Ser	Thr	Tyr	Pro	Gly	Val	Gln		
				325					330					335			
atg	agg	ggg	gtg	ctg	cga	caa	gtg	att	aag	cag	ctc	gat	gca	tct	gag	1056	
Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys	Gln	Leu	Asp	Ala	Ser	Glu		

340										345					350					
atc	aac	gct	cag	cca	gcg	cca	gtc	gtc	gag	aat	gaa	gtt	gcc	aaa	aac	1104				
Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu	Asn	Glu	Val	Ala	Lys	Asn					
355					360					365										
cga	gat	aac	tca	ccc	gtc	att	aca	caa	gct	ttc	ttc	tgg	ccg	cgc	gtg	1152				
Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala	Phe	Phe	Trp	Pro	Arg	Val					
370					375					380										
gga	gag	ttc	ctg	aag	aag	aac	gac	atc	gtc	att	acc	gag	act	gga	aca	1200				
Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val	Ile	Thr	Glu	Thr	Gly	Thr					
385					390					395					400					
gcc	aac	ttt	ggc	atc	tgg	gat	act	aag	ttt	ccc	tct	ggc	gtt	act	gcg	1248				
Ala	Asn	Phe	Gly	Ile	Trp	Asp	Thr	Lys	Phe	Pro	Ser	Gly	Val	Thr	Ala					
405					410					415										
ctt	tct	cag	gtc	ctt	tgg	gga	agc	att	ggg	tgg	tcc	gtt	ggg	gcc	tgc	1296				
Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	Trp	Ser	Val	Gly	Ala	Cys					
420					425					430										
caa	gga	gcc	gtt	ctt	gca	gcc	gcc	gat	gac	aac	agc	gat	cgc	aga	act	1344				
Gln	Gly	Ala	Val	Leu	Ala	Ala	Ala	Asp	Asp	Asn	Ser	Asp	Arg	Arg	Thr					
435					440					445										
atc	ctc	ttt	gtt	ggg	gat	ggc	tca	ttc	cag	ctc	act	gct	caa	gaa	ttg	1392				
Ile	Leu	Phe	Val	Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Leu					
450					455					460										
agc	aca	atg	att	cgt	ctc	aag	ctg	aag	ccc	atc	atc	ttt	gtc	atc	tgc	1440				
Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro	Ile	Ile	Phe	Val	Ile	Cys					
465					470					475					480					
aac	gat	ggc	ttt	acc	att	gaa	cga	ttc	att	cac	ggc	atg	gaa	gcc	gag	1488				
Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile	His	Gly	Met	Glu	Ala	Glu					
485					490					495										
tac	aac	gac	atc	gca	aat	tgg	gac	ttc	aag	gct	ctg	gtt	gac	gtc	ttt	1536				
Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys	Ala	Leu	Val	Asp	Val	Phe					
500					505					510										
ggc	ggc	tct	aag	acg	gcc	aag	aag	ttc	gcc	gtc	aag	acc	aag	gac	gag	1584				
Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala	Val	Lys	Thr	Lys	Asp	Glu					
515					520					525										
ctg	gac	agc	ctt	ctc	aca	gac	cct	acc	ttt	aac	gcc	gca	gaa	tgc	ctc	1632				
Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe	Asn	Ala	Ala	Glu	Cys	Leu					
530					535					540										
cag	ttt	gtc	gag	cta	tat	atg	ccc	aaa	gaa	gat	gct	cct	cga	gca	ttg	1680				
Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu	Asp	Ala	Pro	Arg	Ala	Leu					
545					550					555					560					
atc	atg	acg	gca	gaa	gct	agc	gcg	agg	aac	aat	gcc	aag	aca	gag	taa	1728				
Ile	Met	Thr	Ala	Glu	Ala	Ser	Ala	Arg	Asn	Asn	Ala	Lys	Thr	Glu	*					
565					570					575										

<210> 24
 <211> 575
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 24
 Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp
 1 5 10 15
 Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser
 20 25 30
 Ile His Gly Leu Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu
 35 40 45
 Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
 50 55 60
 Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
 65 70 75 80
 Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala
 85 90 95
 Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro
 100 105 110
 Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly
 115 120 125
 Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys
 130 135 140
 Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp
 145 150 155 160
 His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met
 165 170 175
 Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys
 180 185 190
 Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala
 195 200 205
 Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro
 210 215 220
 Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu
 225 230 235 240
 Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro
 245 250 255
 Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val
 260 265 270
 Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu
 275 280 285
 Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn
 290 295 300
 Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu
 305 310 315 320
 His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln
 325 330 335
 Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu
 340 345 350
 Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn

44